A33. Genetic diversity of *Gracilaria changii* and *Gracilaria edulis* (Gracilariaceae, Rhodophyta) in Malaysian waters

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Gracilaria is the second largest genus of red algae that is widely distributed from the sub-boreal to tropical waters, and is endemic to the Southeast Asian countries. *G. changii* and *G. edulis* are potential species for commercialization in Malaysia as they have high yields of good quality agar with high gel strength for production of agarose and food grade agar. However, regular sampling at various coastal areas in Peninsular Malaysia has indicated that the wild populations of these species are decreasing. The information on intraspecific genetic diversity of this economically important species is still rudimentary despite its potential commercialization. In this study, the mitochondrial cytochrome oxidase subunit 1 gene (*cox*1) was employed to infer the intraspecific genetic diversity of Malaysian *G. changii* and *G. edulis*. Eight mitochondrial haplotypes (C1-C8) were revealed from 243 specimens of *G. changii* with nucleotide differences ranging from 0-6 bp over 923bp. Eleven (E1-E11) mitochondrial haplotypes were identified from 75 specimens of *G. edulis* varying from 0-11 bp over 846 bp. Results have shown that haplotype C1 and haplotype E1 were the basal haplotypes of *G. changii* and *G. edulis*, respectively. Populations at Morib, Selangor or Teluk Pelanduk, Negeri Sembilan, were suggested as probable ancestral population of *G. changii*, and populations at Batu Tengah, Malacca, as the ancestral population of *G. edulis*. The present study showed that *cox*1 gene is a highly divergent genetic marker. This marker is applicable to resolve intraspecies genetic variation and phylogeographic structure for these ecologically and economically important species.